

SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> Nucleotide sequences which code for the metF gene

<130> 000363 BT

<140>

10 <141>

<160> 4

<170> PatentIn Ver. 2.1

15

<210> 1

<211> 1551

<212> DNA

<213> Corynebacterium glutamicum

20

<220>

<221> CDS

<222> (299)..(1345)

<223> metF gene

25

<400> 1

gcgtcaagga cggactcaag tttttcagaa gaattcttat ggccttgccg cgccaggaaa 60

ccagcccacg cataaagagg acggattccg tttcctccat tgagcacgaa actgcgaaga 120

tgggccacag catctgtgac aggagcgccg atatcagcaa ttgttagctc ttgagcatcg 180

aggaactgcg tcaaacgata tcgcacgacc tccggaaatt tgtcgaggtc aaggtcatgg 240

gcatcgaaaac tgctcaagga gacgtccttc aatcgaatag ggggatgctg gctgaatt 298

ttg gtg gag gtg aat aaa tgc cag agg cag tcc caa caa aac act ctc 346

Met Val Glu Val Asn Lys Cys Gln Arg Gln Ser Gln Gln Asn Thr Leu

1

5

10

15

40

atc aca cta aga tac cca ggc atg tcc cta acg aac atc cca gcc tca 394

Ile Thr Leu Arg Tyr Pro Gly Met Ser Leu Thr Asn Ile Pro Ala Ser

20

25

30

45

tct caa tgg gca att agc gac gtt ttg aag cgt cct tca ccc ggc cga 442

Ser Gln Trp Ala Ile Ser Asp Val Leu Lys Arg Pro Ser Pro Gly Arg

35

40

45

50

gta cct ttt tct gtc gag ttt atg cca ccc cgc gac gat gca gct gaa 490

Val Pro Phe Ser Val Glu Phe Met Pro Pro Arg Asp Asp Ala Ala Glu

50

55

60

gag cgt ctt tac cgc gca gca gag gtc ttc cat gac ctc ggt gca tcg 538

Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp Leu Gly Ala Ser

65

70

75

80

55

ttt gtc tcc gtg act tat ggt gct ggc gga tca acc cgt gag aga acc 586

Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr Arg Glu Arg Thr

85

90

95

60

tca cgt att gct cga cga tta gcg aaa caa ccg ttg acc act ctg gtg 634

Ser	Arg	Ile	Ala	Arg	Arg	Leu	Ala	Lys	Gln	Pro	Leu	Thr	Thr	Leu	Val	
			100					105					110			
cac	ctg	acc	ctg	gtt	aac	cac	act	cgc	gaa	gag	atg	aag	gca	att	ctt	682
His	Leu	Thr	Leu	Val	Asn	His	Thr	Arg	Glu	Glu	Met	Lys	Ala	Ile	Leu	
		115					120					125				
cgg	gaa	tac	cta	gag	ctg	gga	tta	aca	aac	ctg	ttg	gcg	ctt	cga	gga	730
Arg	Glu	Tyr	Leu	Glu	Leu	Gly	Leu	Thr	Asn	Leu	Leu	Ala	Leu	Arg	Gly	
		130				135					140					
gat	ccg	cct	gga	gac	cca	tta	ggc	gat	tgg	gtg	agc	acc	gat	gga	gga	778
Asp	Pro	Pro	Gly	Asp	Pro	Leu	Gly	Asp	Trp	Val	Ser	Thr	Asp	Gly	Gly	
					150					155					160	
ctg	aac	tat	gcc	tct	gag	ctc	atc	gat	ctt	att	aag	tcc	act	cct	gag	826
Leu	Asn	Tyr	Ala	Ser	Glu	Leu	Ile	Asp	Leu	Ile	Lys	Ser	Thr	Pro	Glu	
				165					170					175		
ttc	cgg	gaa	ttc	gac	ctc	ggc	atc	gcc	tcc	ttc	ccc	gaa	ggg	cat	ttc	874
Phe	Arg	Glu	Phe	Asp	Leu	Gly	Ile	Ala	Ser	Phe	Pro	Glu	Gly	His	Phe	
			180					185					190			
cgg	gcg	aaa	act	cta	gaa	gaa	gac	acc	aaa	tac	act	ctg	gcg	aag	ctg	922
Arg	Ala	Lys	Thr	Leu	Glu	Glu	Asp	Thr	Lys	Tyr	Thr	Leu	Ala	Lys	Leu	
		195					200					205				
cgt	gga	ggg	gca	gag	tac	tcc	atc	acg	cag	atg	ttc	ttt	gat	gtg	gaa	970
Arg	Gly	Gly	Ala	Glu	Tyr	Ser	Ile	Thr	Gln	Met	Phe	Phe	Asp	Val	Glu	
		210				215					220					
gac	tac	ctg	cga	ctt	cgt	gat	cgc	ctt	gtc	gct	gca	gac	ccc	att	cat	1018
Asp	Tyr	Leu	Arg	Leu	Arg	Asp	Arg	Leu	Val	Ala	Ala	Asp	Pro	Ile	His	
					230				235						240	
ggt	gcg	aag	cca	atc	att	cct	ggc	atc	atg	ccc	att	acc	gag	ctg	cgg	1066
Gly	Ala	Lys	Pro	Ile	Ile	Pro	Gly	Ile	Met	Pro	Ile	Thr	Glu	Leu	Arg	
				245					250					255		
tct	gtg	cgt	cga	cag	gtc	gaa	ctc	tct	ggc	gct	caa	ttg	ccg	agc	caa	1114
Ser	Val	Arg	Arg	Gln	Val	Glu	Leu	Ser	Gly	Ala	Gln	Leu	Pro	Ser	Gln	
			260					265					270			
cta	gaa	gaa	tca	ctt	gtt	cga	gct	gca	aac	ggc	aat	gaa	gaa	gcg	aac	1162
Leu	Glu	Glu	Ser	Leu	Val	Arg	Ala	Ala	Asn	Gly	Asn	Glu	Glu	Ala	Asn	
		275					280					285				
aaa	gac	gag	atc	cgc	aag	gtg	ggc	att	gaa	tat	tcc	acc	aat	atg	gca	1210
Lys	Asp	Glu	Ile	Arg	Lys	Val	Gly	Ile	Glu	Tyr	Ser	Thr	Asn	Met	Ala	
		290				295					300					
gag	cga	ctc	att	gcc	gaa	ggc	gcg	gaa	gat	ctg	cac	ttc	atg	acg	ctt	1258
Glu	Arg	Leu	Ile	Ala	Glu	Gly	Ala	Glu	Asp	Leu	His	Phe	Met	Thr	Leu	
					310					315					320	

aac ttc acc cgt gca acc caa gaa gtg ttg tac aac ctt ggc atg gcg 1306
 Asn Phe Thr Arg Ala Thr Gln Glu Val Leu Tyr Asn Leu Gly Met Ala
 325 330 335

5 cct gct tgg gga gca gag cac ggc caa gac gcg gtg cgt taagccctct 1355
 Pro Ala Trp Gly Ala Glu His Gly Gln Asp Ala Val Arg
 340 345

10 taggaatcat gaagggggag ggcgggtgatc aatacggcaa acggccgttg atccccgtca 1415
 aacctaact gcctgagcaa gtcagtgaag ccgagagagc gatacaggct aaacgcattg 1475
 ttgcctcat cgtcgacctc ggggtgtagac aaaatggcaa aagtgttttg tttgtctttt 1535

15 aacagttcat gcatca 1551

20 <210> 2
 <211> 349
 <212> PRT
 <213> Corynebacterium glutamicum

25 <400> 2
 Met Val Glu Val Asn Lys Cys Gln Arg Gln Ser Gln Gln Asn Thr Leu
 1 5 10 15
 Ile Thr Leu Arg Tyr Pro Gly Met Ser Leu Thr Asn Ile Pro Ala Ser
 20 25 30
 Ser Gln Trp Ala Ile Ser Asp Val Leu Lys Arg Pro Ser Pro Gly Arg
 35 40 45
 Val Pro Phe Ser Val Glu Phe Met Pro Pro Arg Asp Asp Ala Ala Glu
 50 55 60
 35 Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp Leu Gly Ala Ser
 65 70 75 80
 Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr Arg Glu Arg Thr
 40 85 90 95
 Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu Thr Thr Leu Val
 100 105 110
 45 His Leu Thr Leu Val Asn His Thr Arg Glu Glu Met Lys Ala Ile Leu
 115 120 125
 Arg Glu Tyr Leu Glu Leu Gly Leu Thr Asn Leu Leu Ala Leu Arg Gly
 130 135 140
 50 Asp Pro Pro Gly Asp Pro Leu Gly Asp Trp Val Ser Thr Asp Gly Gly
 145 150 155 160
 Leu Asn Tyr Ala Ser Glu Leu Ile Asp Leu Ile Lys Ser Thr Pro Glu
 55 165 170 175
 Phe Arg Glu Phe Asp Leu Gly Ile Ala Ser Phe Pro Glu Gly His Phe
 180 185 190
 60 Arg Ala Lys Thr Leu Glu Glu Asp Thr Lys Tyr Thr Leu Ala Lys Leu
 195 200 205

	Arg Gly Gly Ala Glu Tyr Ser Ile Thr Gln Met Phe Phe Asp Val Glu	
	210 215 220	
5	Asp Tyr Leu Arg Leu Arg Asp Arg Leu Val Ala Ala Asp Pro Ile His	
	225 230 235 240	
	Gly Ala Lys Pro Ile Ile Pro Gly Ile Met Pro Ile Thr Glu Leu Arg	
	245 250 255	
10	Ser Val Arg Arg Gln Val Glu Leu Ser Gly Ala Gln Leu Pro Ser Gln	
	260 265 270	
	Leu Glu Glu Ser Leu Val Arg Ala Ala Asn Gly Asn Glu Glu Ala Asn	
15	275 280 285	
	Lys Asp Glu Ile Arg Lys Val Gly Ile Glu Tyr Ser Thr Asn Met Ala	
	290 295 300	
20	Glu Arg Leu Ile Ala Glu Gly Ala Glu Asp Leu His Phe Met Thr Leu	
	305 310 315 320	
	Asn Phe Thr Arg Ala Thr Gln Glu Val Leu Tyr Asn Leu Gly Met Ala	
	325 330 335	
25	Pro Ala Trp Gly Ala Glu His Gly Gln Asp Ala Val Arg	
	340 345	
30	<210> 3	
	<211> 46	
	<212> DNA	
	<213> Artificial sequence	
35	<220>	
	<223> Description of the artificial sequence: Primer	
	metF-EVP5	
40	<400> 3	
	gatctaggat ccaaaggagg acaaccatgt ccctaacgaa catccc	46
45	<210> 4	
	<211> 32	
	<212> DNA	
	<213> Artificial sequence	
	<220>	
50	<223> Description of the artificial sequence: Primer	
	metF-EVP3	
	<400> 4	
	gatctactcg agttcttcta gttggetcgg ca	32
55		